



SEQUENCE LISTING

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<120> POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS, THE DNA ENCODING THEM AND THE PROCESS FOR THEIR PREPARATION AND USE

<130> 6816/P63221US0

<140> 09/147,443
<141> 1999-01-21

<150> PCT/EP97/03253
<151> 1997-06-20

<150> EP 96810421.6
<151> 1996-06-24

<160> 79

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Homo sapiens

<220>

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<222> (1)..(375)

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Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn
20 25 30
gcc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45
gca ggt ata tgg ttt gat gga agt aac aaa aac tat gca gac tcc
Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser
50 55 60
aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65 70 75
ctg caa ctg aac agc ctg aga gac gag gac acg gct gtg tat tat

Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gag cga gca gca cgt ggt att tct agg ttc tat tac tac tac atg 336
 Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met
 100 105 110
 gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc cca 375
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 115 120 125

 <210> 2
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 35 40
 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 80
 65 70 75
 Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
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 100 105 110
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 115 120 125

<210> 3
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 gtc acc atc act tgc cgg gca agt cag agc att agg agc cat ttg aat 96
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn

20	25	30	
tgg tat cag cag aaa cca ggg aaa gcc cct aag ttg ctg atc tat ggt Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly 35	40	45	144
gcg tcc act ttg caa agt ggc gtc cca tca agg ttc agt ggc agt ggc Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50	55	60	192
tct ggg gca gtt ttc act ctc acc atc gcc agt cta caa cct gaa gat Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp 65	70	75	240
ttt gca act tac tac tgt caa gag agt tac agt aat cct cta atc acc Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr 85		90	288
ttc ggc caa ggg aca cga ctg gag act aaa Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys 100		105	318

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Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly 35	40	45	
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50	55	60	
Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp 65	70	75	80
Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr 85		90	95
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<220>
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<222> (1)...(375)

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 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser
 20 25 30

 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Glu Leu Trp Val
 35 40 45

 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

 ctc caa atg cgc agt ctg agt gcc gac acg gct gtg tat tac tgt 288
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 gcg aga gac aag gcg gtt cg^g gga att agc agg tac aac tat tac atg 336
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

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 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 6
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 <213> Homo sapiens

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 1 5 10 15

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 20 25 30

 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Glu Leu Trp Val
 35 40 45

 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met

100	105	110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser		
115	120	125

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 <213> Homo sapiens

<220>
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 <222> (1)...(318)

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gtc acc atc act tgc cgg gca agt cag aac att atc cgc tat tta aat	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn	
20 25 30	
tgg tat cag cag aag cca ggg aaa gcc cct agg ctc ctg atc tat ggt	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly	
35 40 45	
gcg tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga	192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
tct ggg aca gat ttc act ctc acc atc agt agt ctg caa cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	
ttt gca act tac tac tgt caa cag agt tac cgt acc cct cca ttc act	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr	
85 90 95	
ttc ggc cct ggg acc aaa gtg gag atc aaa	318
Phe Gly Pro Gly Thr Lys Val Glu Ile Lys	
100 105	

<210> 8
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 <213> Homo sapiens

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20 25 30	
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly	
35 40 45	

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
 85 90 95
 Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 9
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<220>
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 tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct 96
 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60
 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 70 75 80
 ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt 288
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg 336
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110
 gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 10
 <211> 125

<212> PRT
<213> Homo sapiens

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20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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<220>
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<222> (1)..(315)

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5
gtc acc atc acc tgc cgg gca agt cag agt atc atc agg tat ttg aat 96
gca 20 25 30
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
tgg tat cag cac aaa cca gga aaa gcc cct aaa ctc ctc atc ttt gct 144
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala
35 40 45
gca tcg aat ttg caa act ggg gtc cca tcc agg ttc agt ggc agt gga 192
Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
tct ggg aca gat ttc act ctc acc atc agt gac ctg cag cct gag gat 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp
65 70 75 80

ttc gca act tac tac tgt caa cag agt tac agt agg ccg ttc act ttt 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe
85 90 95

315

ggc cggttccacc acc agc ctg gac atc aaa
Gly Arg Gly Thr Ser Leu Asp Ile Lys
100 105

<210> 12
<211> 105
<212> PRT
<213> Homo sapiens

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20 25

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35 40

Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60
50 55

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp 80
65 70 75

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85 90

Gly Arg Gly Thr Ser Leu Asp Ile Lys
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<210> 13
<211> 375
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)...(375)

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cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag cct ggg agg
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tcc tgt ata gcg tct gga ttc acc ctc agg aat tat 96
Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr
20 25 30

gcc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gca ggt ata tgg ttt gat gga agc aac aaa aac tat gca gac tcc gtg	192
Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val	
50	55
55	60
aag ggc cga ttc acc atc tcc aga gac aac tcc aag aac act ctg ttt	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe	
65	70
70	75
ctg cac atg aac agc ctg aga gcc gag gac acg gct aca tat tac tgt	288
Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys	
85	90
90	95
gcg aga gag agg gcg att cgg gga atc agt aga tac aat tac tac atg	336
Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	
100	105
105	110
gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca	375
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115	120
120	125

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<213> Homo sapiens

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10	15
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20	25
30	
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35	40
40	45
Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val	
50	55
55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe	
65	70
70	75
80	
Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys	
85	90
90	95
Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	
100	105
105	110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser	
115	120
120	125

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gtc acc atc act tgc cgg gca agt cag agc att cga agc tct tta aat 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn
20 25 30
tgg tat cag cag aaa cca ggg aaa gcc cct aaa gtc ctg atc tat gct 144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala
35 40
gca tcc agt ttg caa agt ggg gtc cca tcc agg ttc agt ggc aga gga 192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly
50 55 60
tct ggg aca gat ttc act ctc acc atc agc agt ctg cag cct gaa gat 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80
ttt gcg act tat tat tgt caa cag agt tcc agt tcc tcg tgg acg ttc 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Trp Thr Phe
85 90 95
ggc caa ggg acc aag gtg gaa atc aaa 315
Gly Gln Gly Thr Lys Val Glu Ile Lys
100

<210> 16

<211> 105

<212> PRT

<213> Homo sapiens

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20 25 30
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala
35 40 45
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly
50 55 60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Trp Thr Phe
85 90 95
Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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 <213> Homo sapiens

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 tcc ctg aga ctt tcc tgt gca gcg tct gga ttc agt ttc aat agc cat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His
 20 25 30

 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Leu Glu Trp Val
 35 40 45

 gca ttt ata tgg ttt gat ggc agt aat aaa tac tat gca gac tcc gtg 192
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

 aag ggc cga ttc acc atc acc aga gac aac tcc aag aac acg ctg tat 240
 Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtc tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 gcg aga gag acc tca gta agg cta ggg tat agc cgc tac aat tac tac 336
 Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr
 100 105 110

 atg gac gtc tgg ggc aaa ggg acc acg gtc acc atc tcg tca 378
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 115 120 125

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<213> *Homo sapiens*

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 35 40 45
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50	55	60	
Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr			
100	105	110	
Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser			
115	120	125	

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<211> 318
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (1)..(318)

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Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1           5           10          15

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gtc acc atc act tgc cgg gca agt cag agc att agg agc cat ttg aat
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn
 20 25 30

tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
35 40 45

gca tcc agt ttg caa ggt ggg gtc cca tca agg ttc agt ggc agt gga
 Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt gca act tat tac tgt caa cag agt tac agg gcc cct cag tgt acg
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr
85 90 95

318

ttc ggc caa ggg acc aag gtg gaa atc aaa	
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
100	105

<210> 20
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<213> *Homo sapiens*

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 20 25 30
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45
 Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Arg Ala Pro Gln Trp Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 21
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(375)

<400> 21
 cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
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 1 5 10 15
 tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ctc agg agt tat 96
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60
 aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg gtc tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr
 65 70 75 80
 ctg caa atg aac agc ctg aga gcc gat gac acg gct gta tat tat tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gag aag gcg ctt cg gga atc agc aga tac aac tat tac ctg 336
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu

100

105

110

375

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 22
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 22
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 23
 <211> 333
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(333)

<400> 23
 gtg gtg act cag cca ccc tca gcg tct ggg acc ccc gga cag agg gtc 48
 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
 1 5 10 15
 acc atc tct tgt tct gga agc aac tcc atc ctt gga agt aag tat gta 96
 Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val
 20 25 30
 tac tgg tac cag aaa ctc cca gga acg gcc ccc aaa ctc ctc atc tat
 Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
 35 40 45 144

aag aat gat cag cgg ccc tca ggg gtc tct gac cga ttc tct ggc tcc	192
Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser	
50 55 60	
aag tct ggc acc tcg gcc tcc ctg gcc atc agt ggg ctc cgg tcc gag	240
Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu	
65 70 75 80	
gat gag gct gac tat tac tgt gca cca tgg gat gcc aac ctg ggt ggc	288
Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly	
85 90 95	
ccg gtg ttc ggc gga ggg acc aag ctg acc gtc cta agt cag ccc	333
Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro	
100 105 110	

<210> 24
<211> 111
<212> PRT
<213> Homo sapiens

<400> 24	
Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val	
1 5 10 15	
Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val	
20 25 30	
Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr	
35 40 45	
Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser	
50 55 60	
Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu	
65 70 75 80	
Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly	
85 90 95	
Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro	
100 105 110	

<210> 25
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(375)

<400> 25	48
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Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly	
1 5 10 15	

tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser	96		
20	25	30	
ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	144		
35	40	45	
gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val	192		
50	55	60	
aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr	240		
65	70	75	80
ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys	288		
85	90	95	
gcg aga gac aag gcg gtt cg gga att agc agg tac aac tat tac atg Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	336		
100	105	110	
gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser	375		
115	120	125	

<210> 26
<211> 125
<212> PRT
<213> *Homo sapiens*

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
20 25 30

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110

Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
115								120				125

<210> 27
<211> 312
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(312)

<400> 27	48
gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga	
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
gtc acc atc act tgc cgg aca agt cag acc att agc aga aat tta aat	96
Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn	
20 25 30	
tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	
aca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga	192
Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
tct ggg aca gat ttc act ctc acc atc aat agt cta caa cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp	
65 70 75 80	
ttt gca act tac tac tgt caa cag agt tac act acc cct tcg ttc ggc	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Pro Ser Phe Gly	
85 90 95	
caa ggg acc aag gtg gaa atc aaa	312
Gln Gly Thr Lys Val Glu Ile Lys	
100	

<210> 28
<211> 104
<212> PRT
<213> Homo sapiens

<400> 28	
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn	
20 25 30	
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	
Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp	

65

70

75

80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly
 85 90 95

Gln Gly Thr Lys Val Glu Ile Lys
 100

<210> 29
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(375)

<400> 29 48
 cag gtg aaa ctg ctc gag tct ggg gga ggc ttg gtc cag ccg ggg ggg
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ttc agg agt tat 96
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg ctc tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
 65 70 75 80

ctg caa atg aat agc ctg aga gcc gag gac acg gct gta tat tat tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg 336
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110

gac gtc tgg ggc aag ggg gcc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser
 115 120 125

<210> 30
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 30
 Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly

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Arg			
Leu			
Ser			
Cys			
Val			
Ala			
Ser			
Gly			
Phe			
Thr			
Phe			
Arg			
Ser			
Tyr			
20			
Ser			
Leu			
Arg			
Leu			
Ser			
Cys			
Val			
Ala			
Ser			
Gly			
Phe			
Thr			
Phe			
Arg			
Ser			
Gly			
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Gly			
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Asn			
Lys			
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Tyr			
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Phe			
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Asn			
Lys			
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Phe			
Ile			
Trp			
Phe			
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Gly			
Ser			
Asn			
Lys			
Gly			
Tyr			
Val			
Asp			
Ser			
Val			
Asp			
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Ser			
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Phe			
Ile			
Trp			
Phe			
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Gly			
Ser			
Asn			
Lys			
Gly			
Tyr			
Val			
Asp			
Ser			
Val			
Asp			
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Asp			
Asn			
Ser			
Lys			
Gly			
Tyr			
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Asp			
Ser			
Val			
Asp			
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Ser			
Ala			
Phe			
Ile			
Trp			
Phe			
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Gly			
Ser			
Asn			
Lys			
Gly			
Tyr			
Val			
Asp			
Ser			
Val			
Asp			
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Phe			
Ile			
Trp			
Phe			
Asp			
Gly			
Ser			
Asn			
Lys			
Gly			
Tyr			
Val			
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Ser			
Val			
Asp			
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Ser			
Ala			
Phe			
Ile			
Trp			
Phe			
Asp			
Gly			
Ser			
Asn			
Lys			
Gly			
Tyr			
Val			
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Ser			
Val			
Asp			
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Ser			
Ala			
Phe			
Ile			
Trp			
Phe			
Asp			
Gly			
Ser			
Asn			
Lys			
Gly			
Tyr			
Val			
Asp			
Ser			
Val			
Asp			
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Ser			
Ala			
Phe			
Ile			
Trp			
Phe			
Asp			
Gly			
Ser			
Asn			
Lys			
Gly			
Tyr			
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Asp			
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Asp			
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Phe			
Ile			
Trp			
Phe			
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Gly			
Ser			
Asn			
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Tyr			
Leu			
Glu			
Trp			
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Gln			
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Trp			
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Gln			
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Pro			
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Gly			
Tyr			
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Trp			
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Phe			
Ile			
Trp			
Phe			
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Gly			
Ser			
Asn			
Lys			
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Tyr			
Leu			
Glu			
Trp			
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Gln			
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Trp			
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Gln			
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Pro			
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Lys			
Gly			
Tyr			
Leu			
Glu			
Trp			
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Trp			
Phe			
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Trp			
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Gln			
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Pro			
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Asn			
Lys			
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Tyr			
Leu			
Glu			
Trp			
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Gln			
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Trp			
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Gln			
Ala			
Pro			
Gly			
Lys			
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Tyr			
Leu			
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Trp			
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Val			
Trp			
Gly			
Lys			
Gly			
Asp			
Ala			
Thr			
Val			
Thr			
Val			
Ser			
Asn			
Lys			
Gly			
Tyr			
Leu			
Glu			
Trp			
Val			
Arg			
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Val			
Trp			
Gly			
Lys			
Gly			
Asp			
Ala			
Thr			
Val			
Thr			
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Lys			
Gly			
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Trp			
Val			
Arg			
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<210> 31
<211> 318
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (1)..(318)

<400> 31 gtg atg acc cag tct cca tcc tcc ctg tct gca tct ata ggc gac aga Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg 1 5 10 15	48
gtc acc atc act tgc cg ^g gca agt cag agc gtt acc agg tct tta aat Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn 20 25 30	96
tgg tat cag cag aaa cca ggg aaa gcc cct agg ctc cta atc ttt gct Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala 35 40 45	144
g ^c g tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60	192
tct ggg aca gat ttc acc ctc acc atc agc agt ctg caa cct gag gat Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80	240
ttt gga act tac tac tgt caa cag aat tac agg acc cct cag tgg acg Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr 85 90 95	288
ttc ggc caa ggg acc aag gta gaa atc aaa	318

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 32
<211> 106
<212> PRT
<213> Homo sapiens

<400> 32
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn
20 25 30
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala
35 40 45
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80
Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr
85 90 95
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 33
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(378)

<400> 33
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ctc agg agt tat 96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr
20 25 30
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
50 55 60
aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg gtc tat 240

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr
65 70 75 80

ctg caa atg aac agc ctg aga gcc gat gac acg gct gta tat tat tat
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr
85 90 95 288

tgt gcg aga gag aag gcg ctt cg gga atc agc aga tac aac tat tac
Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr
100 105 110 336

ctg gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca
Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125 378

<210> 34
<211> 126
<212> PRT
<213> Homo sapiens

<400> 34
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr
85 90 95

Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr
100 105 110

Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 35
<211> 333
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(333)

<400> 35
gtg gtg act cag gag ccc tca ctg act gtg tcc cca gga ggg aca gtc 48
Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val

1	5	10	15	
act ctc acc tgt gct tcc agc act ggg gca gtc acc agg ggt tac tat Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr				96
25				30
cca aac tgg ttc cag cag aag cct gga caa gca ccc agg gca ctg att Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile				144
40				45
tat agt aca aac aaa aaa cac tcc tgg acc cct gcc cggt ttc tca ggc Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly				192
55				60
tcc ctc ctt ggg ggc aaa gct gcc ctg aca ctg tca ggt gtg cag cct Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro				240
70				75
				80
gaa gac gag gct gaa tat tac tgc ctg ctc tac tat ggt ggt gct caa Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln				288
85				90
				95
ctc gta ttc ggc gga ggg acc aag ctg acc gtc cta cgt cag ccc Leu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro				333
100				105
				110

<210> 36
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 36	1	5	10	15	
Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val					
20					25
					30
Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr					
35					40
					45
Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile					
50					55
					60
Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly					
65					70
					75
Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro					
85					90
					95
Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln					
100					105
					110

<210> 37
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
<221> CDS
<222> (1)...(375)

<400> 37 48
cag gtg aaa ctg ctc gag tcg ggg gga ggc gtg gtc cag ccg ggg ggg
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct 96
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
20 25 30
ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
50 55 60
aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
65 70 75 80
ctc caa atg cgc agt ctg agt gcc gac acg gct gtg tat tac tgt 288
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
gcg aga gac aag gcg gtt cg^g gga att agc agg tac aac tat tac atg 336
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110
gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 38
<211> 125
<212> PRT
<213> Homo sapiens

<400> 38
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 39
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(315)

<400> 39
gtg ttg acc cag tct cca tcc tcc ctg tct gca tct ata cga gac aga 48
Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg
1 5 10 15

gtc acc atc act tgc cgg gca agt cag aac att ggc agt tat tta aat 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn
20 25 30

tgg tat cag cac aaa cca ggg aca gcc cct aaa ctc ctg atc tat gct 144
Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala
35 40 45

gta tcc gct ttg caa agt ggg gtc cca tcg agg ttc agt ggc agt aga 192
Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg
50 55 60

tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

ttt gca act tac tac tgt caa cag agt tac agt ccc ccg tac act ttc 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe
85 90 95

ggc cag ggg acc aac ctg cag atc aaa 315
Gly Gln Gly Thr Asn Leu Gln Ile Lys
100 105

<210> 40
<211> 105
<212> PRT
<213> Homo sapiens

<400> 40
Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn

20

25

30

Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45

Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Pro Pro Tyr Thr Phe
 85 90 95

Gly Gln Gly Thr Asn Leu Gln Ile Lys
 100 105

<210> 41
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(375)

<400> 41 48
 cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga gtc gcc tgt gta gcg tct gga ttc acc ttc agg aat ttt 96
 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt 192
 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Asp Ser Val
 50 55 60

aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat 240
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt 288
 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gag aag gcg gtt cgg gga att agt aga tac aac tac tac atg 336
 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 42
<211> 125
<212> PRT
<213> Homo sapiens

<400> 42
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 43
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(315)

<400> 43
gtg atg acc cag tct cca tcc tcc ctg tct gca tct gtg gga gac aga 48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15
gtc acc atc act tgc cgg gca agt cag agc att atc aac aat tta aat 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn
20 25 30
tgg tat cag cag aaa cca ggc aaa gcc cct gaa ctc ctg atc tat gct 144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala
35 40 45
gca tcc agt ttg caa agt ggg gtc cct tca agg ttc cgt ggc agt gga 192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly
50 55 60

tct ggg aga gat ttc act ctc acc gtc acc agt ctg caa cct gaa gat 240
Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp
65 70 75 80

ttt gca act tac tac tgt caa cag agt tac agt acc ctg tgg acg ttc 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe
85 90 95

ggc caa ggg acc aag gtg gaa atc aaa 315
Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 44
<211> 105
<212> PRT
<213> Homo sapiens

<400> 44
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly
50 55 60

Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe
85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 45
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(375)

<400> 45 48
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ttc agg agt tat 96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

ggc atg cac tgg gtc cgc cag gct cca aag ggc ctg gag tgg gtg	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35	40
40	45
gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg	192
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val	
50	55
55	60
aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac acg ctc tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65	70
70	75
ctg caa atg aag agc ctg aqa gag gac acg gct gta tat tat tgt	288
Cys Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr	
85	90
90	95
gcg aga gag aag ggc ctt cgg gga atc agt aga tac aac tat tac ctg	336
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu	
100	105
105	110
gac gtc tgg ggc aag qgg acc acg gtc acc gtc tcc tca	375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser	
115	120
120	125

<210> 46
<211> 125
<212> PRT
<213> Homo sapiens

<400> 46	
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly	
1	5
10	15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr	
20	25
25	30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35	40
40	45
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val	
50	55
55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65	70
70	75
Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85	90
90	95
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu	
100	105
105	110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser	
115	120
120	125

<210> 47
<211> 315
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(315)

<400> 47
gtg atg acc cag tct cca ttc tcc ctg tct gca tct gta gga gac aga 48
Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15
gtc acc atc act tgc cg gca agt cag aac att agg agt ttt tta agt 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser
20 25 30
tgg tat cag cag aaa cca ggg aca gcc cct aag ctc ctg atc tat gct 144
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala
35 40 45
gca tcc agg ttg caa agt ggg gtc cca tca agg ttc agt ggc agt ggg 192
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
tct ggg aca gat ttc act ctc acc atc agc act ctg caa cct gaa gat 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp
65 70 75 80
ttt gcg act tac tac tgt caa cag agt tac agt gcc cct tgg acg ttc 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe
85 90 95
ggc caa ggg acc aag ctg gaa atc aaa 315
Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 48

<211> 105

<212> PRT

<213> Homo sapiens

<400> 48
Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser
20 25 30
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala
35 40 45
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp
65 70 75 80
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe
85 90 95

Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 49
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(375)

<400> 49 48
cag gtg aaa ctg ctc gag tct ggg gga ggc gtc cag ccg ggg ggg
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc tcc agg agt tat 96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr
20 25 30
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
50 55 60
aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac acg ctc tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
ctg caa atg aag agc ctg aga gcc gag gac acg gct gta tat tat tgt 288
Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg 336
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
100 105 110
gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 50
<211> 125
<212> PRT
<213> Homo sapiens

<400> 50
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 51
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(315)

<400> 51 48
 gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15
 gtc acc atc act tgc cgg gca agt cag agc att agc agc tat tta aat 96
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
 20 25 30
 tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45
 gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
 tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 ttt gca act tac tac tgt caa cag agt tac agt acc cga ttc act ttc 288
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe
 85 90 95
 ggc cct ggg acc aaa gtg gat atc aaa 315
 Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 52

<211> 105
<212> PRT
<213> Homo sapiens

<400> 52
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
20 25 30
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
35 40 45
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe
85 90 95
Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 53
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(384)

<400> 53
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag cct ggg agg 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
tcc ctg aga ctt tcc tgt gca gcg tct gga ttt acc ttc agt agc tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
gca gat ata tgg ttt gat gga ggt aat aaa cat tat gca gac ttc gtg 192
Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val
50 55 60
aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg gtg tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80
cta caa atg aac agc ctg aga gtc gag gac acg gct gtg tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
gct agg gat tac tat agc gtt act aag aaa ctc aga ctc cac tac tac 336
Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr
100 105 110

tac tac atg gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 384
Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 54
<211> 128
<212> PRT
<213> Homo sapiens

<400> 54
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg 15
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr
100 105 110
Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 55
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(315)

<400> 55 48
gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15
gtc acc atc act tgc cgg gca agt cag ggc att aga aat gat tta acc 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr
20 25 30

tgg tat cag caa aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala	
35	40
	45
gca tcc aat tta caa agt ggg gtc cca tca agg ttc agc ggc agt gga	192
Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50	55
	60
tct ggc aca gat ttc act ctc acc atc agc agc ctg cag cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65	70
	75
ttt gca act tat tac tgt cta caa gat aac aat ttc ccg tac act ttt	288
Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe	
85	90
	95
ggc cag ggg acc aag ctg gag atc aaa	315
Gly Gln Gly Thr Lys Leu Glu Ile Lys	
100	105

<210> 56
<211> 105
<212> PRT
<213> Homo sapiens

<400> 56	
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1	5
	10
Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr	
20	25
	30
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala	
35	40
	45
Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50	55
	60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65	70
	75
Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe	
85	90
	95
Gly Gln Gly Thr Lys Leu Glu Ile Lys	
100	105

<210> 57
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(375)

<400> 57 48
 cag gtg aaa ctg ctc gag tct ggg gga ggc gtc cag ccg ggg ggg
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga gtc gcc tgt gta gcg tct gga ttc acc ttc agg aat ttt 96
 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Leu Glu Trp Val
 35 40 45
 gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt 192
 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60
 aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat 240
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt 288
 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gag aag gcg gtt cgg gga att agt aga tac aac tac tac atg 336
 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110
 gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 58
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 58
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Ser Ser
115 120 125

<210> 59
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(315)

<400> 59 48
gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15
gtc acc atc act tgc cg^g gca agt cag agc att atc aga tat tta aat 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
20 25 30
tgg tat cag cac aaa cca ggg aaa gcc cct aag ctc ctg atc cat act 144
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr
35 40 45
gca tcc agt ttg caa agt ggg gtc ccg tca agg ttc agt ggc agt gta 192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
50 55 60
tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80
ttt gca act tac tac tgt caa cag agt tac act acc ccg tac act ttt 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Pro Tyr Thr Phe
85 90 95
ggc cag ggg acc aag ctg cag atc aaa 315
Gly Gln Gly Thr Lys Leu Gln Ile Lys
100 105

<210> 60
<211> 105
<212> PRT
<213> Homo sapiens

<400> 60
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
20 25 30
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
85 90 95

Gly Gln Gly Thr Lys Leu Gln Ile Lys
100 105

<210> 61

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(375)

<400> 61

cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga gtc gcc tgt gta gcg tct gga ttc acc ttc agg aat ttt 96
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt 192
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
50 55 60

aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat 240
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt 288
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gag aag gcg gtt cgg gga att agt aga tac aac tac tac atg 336
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110

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Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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<211> 125

<212> PRT

<213> Homo sapiens

<400> 62

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
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Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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<212> DNA

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gtc acc atc act tgc cgg gca agt cag agc att atc aga tat tta aat 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
20 25 30

tgg tat cag cac aaa cca ggg aaa gcc cct aag ctc ctg atc cat gct 144
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala
35 40 45

gca tcc agt ttg caa agt ggg gtc ccg tca agg ttc agt ggc agt gta 192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
50 55 60

tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

ttt gca act tac tac tgt caa cag agt tac act acc ccg tac act ttt 288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
85 90 95

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Gly Gln Gly Thr Lys Leu Gln Ile Lys
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1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
85 90 95

Gly Gln Gly Thr Lys Leu Gln Ile Lys
100 105

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<400> 67

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<400> 68
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32

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32

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<400> 70
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32

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27

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35

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56

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<400> 74

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36

<210> 75

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<212> DNA

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<400> 76

tacgcgttgt gacatcgta tgaccaggc tccat

35

<210> 77

<211> 34

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<213> Homo sapiens

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agtgcgtctag ttgcgttgat ttcaagcttg gtcc

34

<210> 78

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<212> DNA

<213> Artificial Sequence

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<210> 79

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<223> Description of Artificial Sequence: Primer

<400> 79

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31